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#### Ford, Vanessa

From:

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Biotechnology Patent Examiner
Office: CM1 8D17

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OM protein - protein search, using sw model

June 7, 2002, 14:20:58; Search time 30.07 Seconds (without alignments) 73.877 Million cell updates/sec Run on:

US-10-054-64752

1 NTTTGVFGLKQDWDGATIKD 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_032802: Database :

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		op					
Result No.	Score	Query Match	Query Match Length DB	03	QI.		Description
-	110	100.0	:			! ! ! ! ! ! ! !	E. canis P30 prote
101	96	87.3	280	20	AAY06948		E. chafeensis OMP-
m	06	81.8				•	Ehrlichia chaffeen
7	90	81.8	-				Ehrlichia chaffeen
S	90	81.8					Variable surface a
9	82	74.5					E. chafeensis p28
	82	74.5					Ehrlichia chaffeen
ω	82	74.5					Ehrlichia chaffeen
თ	82	74.5					Variable surface a
10	, 82	74.5					Ehrlichia chaffeen
11	82	74.5		21	AAB36183		Ehrlichia chaffeen

	the contract of the contract o	2 E. canis P30-	9 Ehrlichia cani	4 E. canis P	2 Ehrlichia chaf	9	86 Ehrlichia	AAU04196 variable surface	AAY71477 Ehrlichia canis	-	8 Cowdria	2 Cowdri	. Major anti	AAW51093 Ehrlichia chaffeen	E. chafeen	AAB36187 Ehrlichia chaffeen	Variable surfa	E. chafee	Variable s		Ehrlichia	Ehrlichia	Ehrlichia	7 Propionibact	6 Arabidopsis	Arabidopsis	11 Arabidopsis	3 Arabidopsis	0 Arabidopsis	2 Arabidopsis	09 Ar	AAG92136 C glutamicum prot
22	2	20	21	20	13	20	21	22	21	20	19	21	22	19	20	21	. 22	50	22	19	71	21	71	55	21	21	21	77	7	21	21	22
280	187	280	280	276	286	286	286	286	278	307	287	287	287	278	278	278	278	. 087	132	133	. 133	133	283	65	240	364	. 365	374	. 375	442	443	806
74.5		ď		œ.	5.1	ψ.			ω,	m.	4	4.	4.	ω,	e.	ω.	ω.	53.6	4			44.5					40.9				40.9	
82	8.7	77	17.	92	71	7.1	71	7.1	70	70	6	59.5	9.	ശ	50	29	59	29	49	49	49	49	4	47.	45	45	45	45	45	45	45	45
175	13	14	. 15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	77

### ALIGNMENTS

AAY06959 standard; Protein; 288 AA. AAY06959;

05-JUL-1999 (first entry)

E. canis P30 protein.

Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog

Ehrlichia canis

W09913720-A1

25-MAR-1999

98WO-US19600. 18-SEP-1998;

(OHIS ) UNIV OHIO STATE

97US-0059353

19-SEP-1997;

Ohashi N, Rikihisa Y;

WPI; 1999-254290/21. N-PSDB; AAX34759.

Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis

Disclosure; Fig 19B; 55pp; English.

MAP1 homologue; variable surface antigen; VSA4; rickettsla;

Ehrlichia chaffeensis VSA4 protein.

14-SEP-1998 (first entry)

AAW51094;

AAW51094 standard; Protein; 280 AA.

AAW51094

1..25
/note= "putative signal peptide"

W09816554-A1

Peptide

97WO-US19044 96US-0733230

17-0CT-1997; 17-OCT-1996;

23-APR-1998.

Location/Qualifiers

Ehrlichia chaffeensis

DNA vaccine

ö

Gaps

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
       The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown.
In AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                   ö
                                                                                                                                                      Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                   Indels
                                                                                                                                                      Score 110; DB 20;
Pred: No. 1 5e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                     AAY06948 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 8B; 55pp; English.
                                                                                                                                                                                      ö
                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          E. chafeensis OMP-iF protein.
                                                                                                                                                                                                             1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                               60 ntttgvfglkgdwdgatikd 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US19600.
                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1999 (first entry)
                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-254290/21.
N-PSDB; AAX34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AA;
                                                                                                               288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09913720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1999
                                                                                                                 Sequence.
                                                                                                                                                                                                                                                                                                                                                  AAY06948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                         AAY06948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the full-length variable surface antigen VSA4 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAP1 (see AAW51089) of Coworia ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95), A claimed composition comprises a nucleic acid (see AAW07176-82) encoding a polypeptide circkettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria.species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Composition costaining nucleic acid encoding rickettsial antigenuseful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                               ganta RR, Mahan SM, McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90; DB 19;
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36188 standard, Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NTTIGVFGLKODWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                   Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                           UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-251232/22.
N-PSDB; AAV07179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              animals
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ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Gaps

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Length 280 Indels

DB 20;

Score 96;

87,3%;

Query Match 87,3%; Best Local Similarity 94.4%; Matches 17; Conservative

1 NTTTGVFGLKQDWDGATI 18 

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Pred. No. 2.5e-07; 1; Mismatches 0;

us-10-054-647-2.rag

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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettstal disgases caused by a organism of Rickettsia sp. Ehrlichia sp. Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatum genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and against designated map 2, Ihworf3, 4hworf1, 18hworf1 and are used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                           McGuire TC;
                                                                                                                      najor antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                         Mahan SM, McGuire
re WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3e-06;
hes 1; Indels 0;
                                                                                                      Shrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 90; DB 21; Length 280; 88.9%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                         Ganta RR, Burridge MJ, Mahan
nd AL, Simbl BH, Whitmire WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                     Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Bowle MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                                    99US-0130725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 nttigvfglkgdwdgsti 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NTTTGVFGLKQDWDGATI 18
                                    (first entry)
                                                                                                                                                                                             Shrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                       UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-679675/66.
N-PSDB; AAC68705.
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AA;
                                                                                                                                                                                                                              NO200065063-A2
                                                                                                                                                                                                                                                                                                                                    22-APR-1999;
                                    32-MAR-2001
                                                                                                                                                                                                                                                               02-NOV-2000
AAB36188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                            3qdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
   .g
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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures

Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;

WPI; 2001-424487/45

N-PSDB; AAS07578

97US-0953326.

17-OCT-1997;

Ehrlichia chaffeensis.

US6251872-B1

26-JUN-2001

96US-0733230

.7-0CT-1996;

(UYFL ) UNIV FLORIDA.

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The sequence represents the amino acid sequence of variable surface antigen 4 (VSA4) isolated from Ehrlichia chaffeensis, which ass similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 90; DB 22;
Pred. No. 2.3e-06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                           Example 3; Fig 2A-2B; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06942 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US19600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. chafeensis p28 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.8
Best Local Similarity 88.9
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Ö

Gaps

Major antigenic įrotein; MAP; vaccine; immunogenic; rickettsia; inįection; heartwater; diagnostic; variable surface antigen; VSA.

Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis

23-OCT-2001 (first entry)

AAU04198;

AAU04198 standard; Protein; 280 AA.

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Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                     Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW51095 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                        Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 nttvgvfglkqnwdgsalsn 53
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97US-0059353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                     (OHIS ) UNIV OHIO STATE
                                                                                                       Ohashi'N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shritchia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251232/22.
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                                                                                                                                                                  WPI: 1999-254290/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AA;
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                                                                                                                                                                                             N-PSDB; AAX34742
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19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09816554-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW51095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW51095
ID AAW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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Claim 3; Fig 2B; 39pp; English.

animals

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276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-2000
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                AAB36189
                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                   ö
The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The Er chafeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(8 to 2) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                         Score 82; DB 20; Length 256;
Pred. No. 4e-05;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia chaffeensis VSAS protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid residues. The VSA5 amino acid sequence was deduced from a partial open reading frame (ORFS) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAM51088) of Cowdria rundiantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51081-95) encoding a polypeptide (see AAW51081-95). A chaimed composition comprises a nucleic acid is used, in human or veterinary medicine. In vaccines to protect against Rickettsia. Ehrlichia, maplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis, VSA5, variable surface antigen 5, MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                  Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 19;
Pred. No. 4.3e-05;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis partial VSA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36189 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 47; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  74.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000WO-US10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%
Matches 14; Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-679675/66.
N-PSDB; AAC68706.
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us-10-054-647-2.rag

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Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines condition by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                            276 AA;
                                                                                                                                                                                                                                                            Sequence
8888888888
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74.5%; Score 82; DB 21; Length 2/70.0%; Pred; No. 4.3e-05; Judels 1 NTTTGVFGLKQDWDGATIKD 20 Conservative Query Match Best Local Similarity Matches 14; Conserv ö

59 nttvgvfglkgnwdgsalsn 78 a

AAU04199 standard; Protein; 276 AA.

(first entry) 23-OCT-2001

AAU04199;

Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.

Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA

Ehrlichia chaffeensis

US6251872-B1

26-JUN-2001.

17 CCT-1997;

96US-0733230. 17-0CT-1996;

(UYEL ) UNIV FLORIDA

Nyika A; McGuire TC, Burridge MJ, SM, Bowie MV, Alleman AR; Barbet AF, Ganta RR, McGu Rurangirwa FR, Mahan SM,

WPI; 2001-424487/45. N-PSDB; AAS07578. New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures

Example 3; Fig 2A-2B; 30pp; English.

The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to traise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is 

276 AA; Sequence

Gaps ö Length 276; 3; Indels Score 82; DB 22; Pred. No. 4.3e-05; 3; Mismatches 3; 74.5%; 70.0%; Query Match 74.5 Best Local Similarity 70.0 Matches 14; Conservative

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20 1 NTTTGVFGLKQDWDGATIKD

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AAW51089 standard; Protein; 280 AA. AAW51089 RESULT

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Gaps

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Length 276;

AAW51089;

14-SEP-1998 (first entry)

Ehrlichia chaffeensis major antigenic protein 1 (MAP1).

MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine.

Ehrlichia chaffeensis

WO9816554-A1.

23-APR-1998.

97WO-US19044. 17-OCT-1997;

96US-0733230

17-0CT-1996;

(UYFL ) UNIV FLORIDA.

Ganta RR, Mahan SM, McGuire TC; Barbet AF, Burridge MJ, Nyika A, Rurangirwa FR;

WPI; 1998-251232/22. N-PSDB; AAV07177.

Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or animals

Claim 3; Page 18-19; 39pp; English

of Ehrlichia chaffeensis. It is encoded by the MAPI gene (see AAV07177).

AL claimed composition comprises a nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51088-99) that ellicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Ehrlichia, Annaplasma and Cowdria species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed). This polypeptide comprises the major antigen protein 1 gene (MAP1) 

280 AA; Sequence

Gaps ö Length 280; 74.5%; Score 82; DB 19; Length 28 70.0%; Pred. No. 4.4e-05; ive 3; Mismatches 3; Indels Best\_Local Similarity 70.0% Matches 14; Conservative Query Match

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1 NTTTGVFGLKQDWDGATIKD 20

ö 셤

60 nttvgvfglkqnwdgsaisn 79

Nyika A;

Burridge MJ, , Alleman AR;

RESULT 11

AAB36183

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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia;
Major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 15-17; 30pp; English
                                                                                                                                                                                                                                                                                             McGuire TC, Bo
SM, Bowie MV,
                                                      infection; heartwater; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. chafeensis OMP-1 protein.
                                                                                                                                                                                                                            96US-0733230
                                                                                                                                                                                        97US-0953326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NTTTGVFGLKQDWDGATIKD
                                                                                                                                                                                                                                                                                               Barbet AF, Ganta RR, Mc(
Rurangirwa FR, Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                     Ehrlichia chaffeensis
                                                                                                                                                                                                                                                             (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-424487/45.
N-PSDB; AAS07576.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; dog
                                                                                                                                                                                          17-OCT-1997;
                                                                                                                                                                                                                          17-0CT-1996;
                                                                                                                       US6251872-B1
                                                                                                                                                         26-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY06943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                       Major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06943
     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is given in a specification relating to nucleic acid vaccines containing genes to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The vaccine comprises the major antigenic protein 1 (MAP1) gene or the major antigenic protein 2 (MAP2) gene of rickettsial pathogens. The nucleic acid vaccines can be
                                                                                                                                                                           Ehrlichia chaffeensis; MAP1; major antigenic protein 1; antirickettsial;
vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3;
4hworf1; 18hworf1; 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, lhworf3, 4hworf1, 18hworff1 and addoctf1 and be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ganta RR, Burridge MJ, Mahan SM, McGuire
nd AL, Simbi BH, Whitmire WW, Alleman AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%; Score 82; DB 21; L
70.0%; Pred. No. 4.4e-05;
tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04193 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 35-36; 63pp; English.
                                         AAB36183 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Bowie MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                                                                                      99US-0130725.
                                                                                                                                             Ehrlichia chaffeensis MAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                Shrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 2000-679675/66.
N-PSDB: AAC68700.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AA;
                                                                                                                                                                                                                                                                                 WO200065063-A2
                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1999;
                                                                                                          02-MAR-2001
                                                                                                                                                                                                                                                                                                                   02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                          AAB36183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3;
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The sequence represents the amino acid sequence of major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis. The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 22; Length 280;
Pred. No. 4.4e-05;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06943 standard; Protein; 281 AA.
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(finat entry)

23-OCT-2001

かけてん

AAU04193;

AAU04193 ID AAU0 XX AC AAU0 XX DT 23-0

RESULT 12

9

family and

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Gaps

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Length 280 4; Indels

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The patent relates to homologous 28-kiloDalton (kDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA2, ECa28SA3, ECa28-1 and ECa28-2. These genes are members of a polymorphic multiple gene family and contained in a single locus of 5.592 kb. The 28-kDa proteins are immunoreactive with anti-E. The protein is useful for vaccinating against E. canis infections such as canine ehrlichiosis in dogs.
of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; p01% profile multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettsial disease; serodiagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine ehrlichiosis, also known as canine tropical pancytopaenia, is tick-borne rickettsial disease of dogs. Eca28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis ECa28SA3 30-kDa protein which is post-translationally modified to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia canis immunoreactive protein ECa28SA3
                                                                                                                                               Score 77; DB 20;
Pred. No. 0.00028;
3; Mismatches 4.
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/label- Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                          AAY71479 standard; Protein; 280 AA.
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59 nstvqvfqlkhdwnggtisn 78
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                                                                                                                                Query Match
Best Local Similarity 65.v.,
-hes 13; Conservative
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99US-0261358
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N-PSDB; AAD01294, AAD01295.
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                                                                                                280 AA;
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03-MAR-1999;
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                                                                                                                                                                                                                                                                                                                     The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAVG693-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAVG6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                                                                                              outer membrane proteins from Ehrlichia chaffeensis and
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                                                                                                                                                                                                                                                                                     Disclosure; Fig 3B; 55pp; English.
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es 14; Conservative
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                                                                                              (OHIS ) UNIV OHIO STATE
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                                                                                                                                  Ohashi N, Rikihisa Y;
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                                                                                                                                                                                         N-PSDB; AAX34743
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                   18-SEP-1998;
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Best Local Si
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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RESULT

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mature 28-kDa protein by cleavage of N-terminal signal sequence. ပ္တန္တင္တ

Sequence 280 AA;

0; Gaps Query Match
Best Local Similarity 65.0%; Pred. No. 0.00028;
Matches 13; Conservative 3; Mismatches 4; Indels

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1 NTTTGVFGLKQDWDGATIKD 20 |:| |||||| ||:| || 59 59 nstvgvfglkhdwnggtign 78

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Search completed: June 7, 2002, 14:30:16 Job time: 558 sec

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Sequence 18, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Nylka, Aceme
APPLICANT: Rurangirwa, Fred R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Ehrlichia chaffeensis
US-08-953-326-17
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Les 16, Conservative
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US-08-953-326-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
                                                                                   June 7, 2002, 14:27:08 ; Search time 13.08 Seconds (without alignments) 37.348 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                    lotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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110
1 NTTTGVFGLKQDWDGATIKD 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps

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Score 90; DB 4; Length 280; Pred. No. 4.9e-07; 1; Mismatches 1; Indels

81.8%; 88.9%;

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APPLICANT: McGulre, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Withs, Aceme
APPLICANT: Wahan, Suman M.
ITILE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-167c1
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
SARLIER FILING DATE: 1996-10-17
NUMBER: OS SOFTWARE: Patentin Ver. 2.0
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US-09-034-336-4
US-09-334-336-4
PCT-US93-09782-4
US-08-446-600A-4
US-09-199-637A-363
US-09-413-231-6
US-09-586-165-3
US-08-586-165-3
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Patent No. 6251872
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Ouery Match 74.5%; Score 82; DB Best Local Similarity 70.0%; Pred. No. 9.6e Matches 14; Conservative 3; Mismatches
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APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Nucleic Acid Vaccines Against
Rickettsial Diseases and Methods of Use
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Best Local Similarity 70.0%; Pred. No. 9.5e-06;
Matches 14; Conservative 3; Mismatches
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                                                                                     CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ. ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 18
LENGTH: 276
TYPE: PAT
US-08-953-326-18
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Ganta, Roman Reddy
McGuire, Travis C.
Burridge, Michael J.
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Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
RESISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
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APPLICANT: Rurangirwa. Fred R. APPLICANT: Rurangirwa. Fred R. APPLICANT: Mahan, Suman M. TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 280;
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CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
WUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.0
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CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
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Pred. No.
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EARLIER FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                  Sequence 4, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
                                                                                                                                                                                                                                                                                                                 APPLICANT: McGuire, Travis C. APPLICANT: Burridge, Michael J.
1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 74.5%;
Best Local Similarity 70.0%;
Matches 14; Conservative
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                                                  60 NTTVGVFGLKONWDGSAISN 79
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APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Aravis C.
APPLICANT: Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER PIPLING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 287
                 Sequence 2, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Cowdria ruminantium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                     FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-08-953-326-16
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APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.5; DB 3; Length 287;
Pred. No. 0.043;
1; Mismatches 1; Indels
                                                                                                                                           Query Match 64.5%; Score 71; DB 4; Length 286; Best Local Similarity 66.7%; Pred. No. 0.00059; Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
ARPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Sallwanchik & Sallwanchik : 2421 N.W. 41st Street, Suite A-1 Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08733230 Patent No. 6025338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burridge, Michael J.
Nyika, Aceme
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WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbet, Anthony F. Ganta, Roman Reddy McGuire, Travis C.
                                          TYPE: PRT ORGANISM: Ehrlichia chaffeensis
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80.0%;
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                                                                                                                                                                                                                                                60 NTTVGVFGIEQDWDRCVI 77
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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SEQ ID NO 15
LENGIH: 286
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PPLICANT: Mahan, Suman M.
ITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
ITLE OF INVENTION: Animals and Humans
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                                           Gaps
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Length 287;
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); DB 4; Length 2x
0.043;
ches 1; Indels
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Pred. No. 0.05;
3; Mismatches
                                         1; Mismatches
   Score 59.5;
Pred. No. 0.
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CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1997-10-17
                                                                                                                                                                                                          Sequence 16, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
                                                                                                                                                                                                                                                                                                                              APPLICANT: Burridge, Michael J
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rurangirwa, Fred R. APPLICANT: Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 278
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                                                                                                   62 NTQT-VFGLKKDWDG 75
                                                                               1 NTTIGVEGLKQDWDG 15
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Best Local Similarity
Matches 9; Conserval
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1 NTTTGVFGLKQDWDG 15

Gaps ij

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Sequence 2, Application US/08991942
Patent No. 6015673
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL ONIONALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  36.8%; Score 40.5; DB 2; Length 1025; 42.9%; Pred. No. 2.2e+02; tive 2; Mismatches 7; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/991,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40.5; DB 3;
Pred. No. 2.2e+02;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 NTVSGLMGLKSDGTPWPAVGI 756
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                             1 NTTTGVFGLKQD---WDGATI 18
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Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 amino acids
                                                                                                      1025 amino acids
                    TELEPHONE: (415) 543-96(
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: .
                                                                                                                                                                                                                                                       0uery Match
Best Local Similarity 42.99
Matches 9; Conservative
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-991-942-2
                                                                                                                                                                 , MOLECULE TYPE: protein US-08-304-309-2
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                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-08-991-942-2
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APPLICANT: Nylka, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16/21.
CURRENT APPLICATION WUMBER: US/08/953,326
CURRENT APPLICATION WUMBER: 08/953,326
EARLIER APPLICATION WUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
EARLIER APPLICATION WUMBER: 08/733,230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
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Pred. No. 0.89;
3; Mismatches
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NAME: Smith, Tamothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        Sequence 20, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08304309
Patent No. 5856454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.5%;
                                                                                                                                                                                                                                                         APPLICANT: Burridge, Michael J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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Best Local Similarity 56.2.
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US-08-953-326-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                      60 NPTVALYGLKQDWEG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94105-1493
                                                                                                          JS-08-953-326-20
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US-08-304-309-2
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CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Haemophilus influenzae US-09-268-347-48
                                                                                                                                                                                                                                                    736 NTVSGLMGLKSDGTPWPAVGI 756
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SOFTWARE: Patentin version 3.0
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1025 amino acids
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                                                        MOLECULE TYPE: protein
                     amino acid
                                         linear
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 2048
                                                                             PCT-US95-04567-4
                                                                                                                                                                                                                                                                                                                                                   JS-09-268-347-48
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                          TITLE OF INVENTION: Immunological Materials and Methods for Detecting TITLE OF INVENTION: Dihydropyrimidine Dehydrogenase FILE REFERENCE: 09/138,103 Yoshikubo, et al. CURRENT APPLICATION NUMBER: US/09/138,103A CURRENT FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04567
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UOAB025P-
FELECOMMUNICAȚION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 97114630.3
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,357
FILING DATE: 13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9504567
GENERAL INFORMATION:
APPLICANT:
                                                                           Sequence 2, Application US/09138103A Patent No. 6232448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            736 NTVSGLMGLKSDGTPWPAVGI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NTTTGVFGLKQD---WDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.8%;
nilarity 42.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (512) 418-3000
(713) 789-2679
                                                                                                                                          APPLICANT: Yoshikubo, Takashi
APPLICANT: Hasegawa, Masami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-138-103-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77210
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SEQUENCE CHARACTERISTICS:

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APPLICANT: LOSSINGRE, Sheena M.
TILLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS FILE REFERENCE: 1038-860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: USUDA, Yoshihiro
APPLICANT: MIHARA, Yoshihiro
APPLICANTON: GMP Synthetase and Gene Coding for the Same
FILE REFERENCE: 0010-1101-0
CURRENT APPLICATION NUMBER: US/09/550,338
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: JP 11-114787
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Ouery Match 36.8%; Score 40.5; DB 5; Length 1025; Best Local Similarity 42.9%; Pred. No. 2.2e+02; Matches 9; Conservative 2; Mismatches 7; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 2048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 523;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.8%; Score 40.5; DB 4 Best Local Similarity 39.3%; Pred. No. 5e+02; Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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Search completed: June, 7, 2002, 14:

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GenCore version 4.5
Copyright (c) 1993, - 2000 Compugen Ltd.
```

OM protein - protein search, using sw.model

June 7, 2002, 14:27:58 ; Search time 15.01 Seconds Run on:

US-10-054-647-2

110 1 NTTIGVEGIKQDWDGATIKD 20 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		#P				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
	06	81.8	280	7	JE0217	28k surface antiqe
7	. 82	74.5	276	~	JE0218	surface
'n	71	64.5	286	~	JE0219	
4	59	53,6	278	7	JE0216 .	surface
'n	83	53.6	284	~	140882	ige
9	52	47.3	5188	~	B85547	ble RTX fam
7	52	47.3	5291	Ċ	F90696	
<b>60</b>	51	46.4	1191	۲۷	A53491	a)
6	49	44.5	133	.7	JE0221	28k surface antige
. 10	49	44.5	634	~	F97172	겁
11	47	42.7	540	~	S54586	probable membrane
12	47	42.7	584	?	C48658	c
13	46.5	42.3	267	~	C83242	conserved hypothet
14	46	41.8	261	~	G84057	O
15	45	40.9	.160	7	A75466	
16	45	40.9	756	۲,	T20109	hypothetical prote
17	44	40.0	281	~	AH3012	outer surface prot
18	44	40.0	284	~	, B69945	ᠣ
19	44	40.0	284	~	698271	
20	44	40.0	465		S47738	
21	44	40.0	465	~	F91178	๋ย
22	44	40.0	465	ď	G86024	cytochrome-c perox
23	44	40.0	534	~	C82096	15
24	44	40.0	648	-+	P3BPF6	P3 protein - phage
25	44	40.0	1004	~	JH0470	Na+/K+-exchanging
. 26	43.5	39.5	290	~	S76787	hypothetical prote
27	43	39.1	280	~	D70976	
28	43	39.1	427	7	140167	O)
53	43	39.1	470	<b>(1</b>	JC4098	tetracycline 6-hyd

	probable leucyl am	hypothetical prote	Na+/K+-exchanging	hypothetical prote	rhizobiocin/RTX to	probable phosphoes	conserved hypothet	hypothetical prote	hypothetical prote	probable formate a	probable activatin	probable activatin	hypothetical prote	S-adenosylmethioni	conserved hypothet	dnaA protein - Str	
	G75483	G87276	A56594	C86822	AH3098	A96188	AE0293	AI2476	C72390	S56603	A91296	D86137	T44893	F75379	T08297	A41870	-
	N	~	~	~	N	ď	N	~	~	-	~	~	~	7	~	~	
;	482	681	1037	1649	1944	1990	123	160	224	287	287	287	307	362	413	959	
	39.1	39.1	39.1	39.1	39.1	39.1	38.6	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	
	43	43	43	43	43	43	42.5	42	42	42	42	42	42	42	42	. 42	•
	30	31	32	33	34	35	36	37	38	39	40	41	42	. 43	44	45	

## ALIGNMENTS

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R.Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A.FILLE: Molecular characterization of a 28kDa surface antigen gene family of the tri A.Reference number: JE0216; MUID: 98321180
A.Reference number: JE0217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                       C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 2; Length 280; Pred. No. 1.8e-06;
8k surface antiqen 4 - Ehrlichia chaffensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                           A Molecule type: DNA
A, Residues: 1-280 <RED>
A, Cross-references: GB: AF062761
                                                                   C; Species: Ehrlichia chaffensis
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Gaps 1; Mismatches Conservative Query Match Best Local Similarity Matches 16; Conserv

RESULT JE0218

28k surface antigen 5 - Ehrlichia chaffensis

N;Alternate names: MAP1 C;Species: Ehrlichia chaffensis C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 17-Mar-1999

C; Accession: JE0218 R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R Biochem, Biophys. Res. Commun. 247, 636-643, 1998 A; Title: Molecular characterization of a 28kDa surface antigen gene family of the tri A; Reference number: JE0216; MUID: 98321180

A; Molecule type: DNA A; Accession: JE0218

A; Residues: 1-276 <RED>
A; Cross-references: GB: AF062761

Gaps Length 276; Ouery Match 74.5%; Score 82; DB 2; Length 276 Best Local Similarity 70.0%; Pred. No. 3.1e-05; Matches 14; Conservative 3; Mismatches 3; Indels

ö

1 NTTTGVFGLKQDWDGATIKD 20 ŏ g

59 NTTVGVFGLKQNWDGSAISN 78

- Ehrlichia chaffensis

88k surface antigen 2 7,Alternate names: MAF

Accession: JE0219

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hypothetical protein ECs0542 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (Species: Escherichia (Species: Escherichia (Species: Escherichia (Species: Escherichia (Species: Escherichia (Species: Escherichia coli 0157:H7) and gastalia (Species: Escheri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Itle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                       probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7, substra C;Species: Escherichia coli
C;Species: 16-Feb.2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Čross-references: GB:AE005174; NID:912513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
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A;Cross-references: GB:BA000007; PIDN:BAB33965.1; PID:913360000; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A53491
bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish
C;Species: Squalus acanthias (spiny dogfish)
C;Date: O2-Jun-1994 #sequence_revision O2-Jun-1994 #text_change O2-Mar-2001
C;Accession: A53491
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 37;
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    Indels
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2; Mismatches
    Mismatches
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Pred. No. 3
    ï
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illarity 60.0%;
Conservative
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4906 TTSGVAAMDYDWDGA 4920
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Best Local Similarity 60.0
Matches 9; Conservative
    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TTTGVFGLKQDWDGA 16
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                                                                                   3 TTGVFGLKQDWDG 15
                                                                                                                                                               63 TKAVFGLKKDWDG 75
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary A; Molecule type: DNA
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A.Gene: ECs0542
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    Matches
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R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Blophys. Res. Commun. 247, 636-643, 1998
A; Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe A; Recession: JE0216; MUID: 98321180
                                                                                                                                                                                                                                                                   R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe A;Reference number: JE0216; MUID:98321180
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C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140882; S42827 ***
R;Van Vilet, A.H.; Jongejan, F.; Van Kleef, M.; Van der Zeijst, B.A.
Infect. Immun. 62, 1821-1456, 1994
A;Title: Wolecular cloning, sequence analysis, and expression of the gene encoding the A;Reference number: 140882; MUID:94178956
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C.Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
                                                                                                                                                               C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
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53.6%; Score 59; DB 2 60.0%; Pred. No. 0.12; Mismatches

Query Match 53.6
Best Local Similarity 60.0
Matches 9; Conservative

g

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A;Cross-references: GB:AF062761

1-278 <RED>

A; Residues:

A; Molecule type: DNA

2; Mismatches

1 NTTTGVFGLKQDWDGATI 18 : 60 NTTVGVFGIEQDWDRCVI 77

8

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64.5%;

Query Match
Best Local Similarity 66.7
Matches 12; Conservative

A; Cross-references: GB: AF062761

A, Molecule type: DNA A, Residues: 1-286 <RED>

A; Accession: JE0219

28k surface antigen 3 - Ehrlichia chaffensis

N; Alternate names: MAP1

Status: preliminary; translated from GB/EMBL/DDBJ

Residues:

Genetics:

53.6%; 76.9%;

Query Match Best Local Similarity

Score 51; DB 2; Pred. No. 11; 2; Mismatches

46.4%;

Conservative

Local Similarity les 10; Conserv

Matches

Query Match

A; Accession: A53491

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8k surface antigen 2 - Ehrlichia canis

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), Residues: 1-540 <PEA>
A;Cross-references: EMBL:249704; NID:g825540; PIDN:CAA89777.1; PID:g825545; GSPDB:GNO
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rischoenhals, G.; Whitfield, C.
J. Bacteriol. 175, 5395-5402, 1993
A;Title: Comparative analysis of flagellin sequences from Escherichia coli strains po
A;Reference number: A48658; MUID:93374833
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999
                                                                                                                                                                                             C,Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
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C;Superfamily: flagellin
                                                                                               N;Alternate names: hypothetical protein YM8021.05c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jil-100c 1-20c
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Pred. No. 19;
3; Mismatches
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Pred. No. 21;
3; Mismatches
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R;Pearson, D; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
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66.78;
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Matches 8; Conservative
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199 NTTTGLYGLKTE 210
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Best Local Similarity
Matches 7; Conserv
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J. Bacteriol. 183, 4823-4834, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A.Reference, number: A96900; MUID:21359325; PMID:21359325
R;Xu, J.C.; Lytle, C.; Zhu, T.T.; Payne, J.A.; Benz Jr., E.; Forbush III, B.
Proc. Natl. Acad. Sci.U. D.S.A.; 2010-2205, 1994
A;Title: Molecular cloning and functional expression of the bumetanide-sensitive Na-K-Cl
A;Reference number: A53491; MUID:94181560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: JE0221.
Reddy, G.R.; Sulsona. C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Jochem. Blophys. Res. Commun. 247, 636-643, 1998
Title: Molecular characterization of a 28kba surface antigen gene family of the tribe Reference number: JE0216; MUID:98321180
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: GB:AF062762; NID:93327964; PIDN:AAC26722.1; PID:93327966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Ehrlichia canis
C.Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
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                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1191 <XUA>
A;Cross-references: GB:U05958; NID:g454096; PIDN:AAB60617.1; PID:g454097
C;Superfamily: rat bumetanide-sensitive Na+/K+/C1--cotransport protein
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Score 49; DB 2 Pred. No. 2; 3; Mismatches

44.5%; 56.2%;

Query Match
Best Local Similarity 56.2
Matches 9; Conservative

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RESULT

Score 49; DB 2;

44.5%;

1 NTTTGVFGLKQDWDGATIKD 20

Conservative

Best Local Similarity Matches 10; Conserv

Query Match

Residues: 1-634 <KUR> Status: preliminary

A;Gene: CAC2212

Accession: F97172

Accession: F97172

Mismatches Pred. No. 11;

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Gaps ö

Length 160; Indels

A;Status: preliminary

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A;Cross-references: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g645
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                        Mismatches
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Job time: 180 sec
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50.0%;
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Best Local 7; Conservative
                                                                                                                                 A.Gene: DR0859
A.Map position: 1
C.Keywords: methyltransferase
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A; Residues: 1-160 <WHI>
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R.White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vemathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
coleic Acids Res. 28, 4317-4317, 2000
Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
Reference number: A83650; WUID: 20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Résidués: 1:261.<STO>,
Cross-references: GB:AP001518; GB:BA000004; NID:910175792; PIDN:BAB06982.1; GSPDB:GN00
Experimental source: strain C-125
                                                                                                              P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
                                                                                                                                                                                           TILLE: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06627.1; GSPDB:GN001
A;Experimental source: strain PA01
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served hypothetical protein PA3239 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                          Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Ppothetical protein BH3263 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                           A:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, Y.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kaš, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Ittle: Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 2; Length 261; 
Pred. No. 13; 
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: Bacillus subtilis hypothetical protein ytmP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46.5;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.38;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 NTTFGVLGL---WDPAT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTTTGVFGLKQDWDGAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 64.7
eg 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 DWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
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                                                                                        Accession: C83242
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                                                                                                                                                                                                                                                                              Accession: C83242
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: PA3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: BH3263
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Matches
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 7, 2002, 14:30:38 ; Search time 10.34 Seconds

(without alignments)

74.893 Million cell updates/sec

Title: US-10-054-647-2

Perfect score: 110
Sequence: 1 NTTGVFGLKQDWDGATIKD 20

Perfect score: 110
Sequence: 1 NTTTGVFGLKQDWDGATIKD 20
Scoring table: BLOSUM62 Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	P55013 squalus aca		Q9rw10 deinococcus		P45908 bacillus su	_	P11129 bacteriopha				P50997 canis famil	P39409 escherichia	032960 mycobacteri	P27902 streptomyce	~	Q9k018 neisseria m	Q9jvp2 neisseria m	027139 methanobact		Q9s3q2 porphyromon		escheri	P79775 gallus gall	zymom	Q12882 homo sapien	halob	.007934 bacillus su	~	Q9zjk8 helicobacte		m	Q17361 caenorhabdi	032106 bacillus su
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gr	NKC1_SQUAC	YM8M_YEAST	MENG_DEIRA	K6PF_CAEEL	YOAK_BACSU	YHJA_ECOLI	VP3_BPPH6	ATIA_ARTSF	AROE SYNY3	PYRC_BACCL	A1A1_CANFA	YJJW_ECOLI	YM16_MYCLE	DNAA_STRCO	A1A2_HUMAN	GCST_NEIMB	GCST_NEIMA	YA67_METTH	KIME_RAT	HTPG_PORGI	VP4_ROTGA	YCBS_ECOLI	ANF1_CHICK	PURL_ZYMMO	DPYD_HUMAN	GVM1_HALN1	YRAJ_BACSU	PGHD_URSAR	BIOB_HELPJ	BIOB_HELPY	Y33B_MYCPN	UBPT_CAEEL	AMPA_BACSU
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Query Match Length	1191	540	160	756	284	465	648	1004	290	427	1021	287	307	656	1020	366	368	377	395	684	749	866	196	734	1025	84	120	191	282	282	341	489	200
Query Match	46.4	42.7	40.9	40.9	40.0	40.0	40.0	40.0		39.1	39.1	38.2		38.2		37.7	37.7	37.3		37.3			36.8	36.8	36.8	36.4	36.4		36.4	36.4	36.4	36.4	36.4
Score	51	47	45	45	44	44	44	44	43.5	43	43	42	42	7	42	41.5	41.5	41	. 41	41	41	41	40.5	40.5	40.5	40	40	40	40	40	\$	40	40
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P31627 caprine art P06686 rattus norv	P05023 homo sapien P13607 drosophila P55012 mus musculu	P55011 homo sapien P13508 caenorhabdi	P14563 caenornabdi P24620 micromonosp P40756 rana catesb	097gu2 clostridium P24021 aspergillus
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NV_CAEVG 1A2_RAT	A1A1_HUMAN ATNA_DROME NKC1_MOUSE	KC1_HUMAN LP1_CAEEL	GRM_MICEC	TD_CLOAB US1_ASPOR
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942	1023	1212	1429 105 118	149 267
36.4 36.4	36 36 4.4.4	36.4	35.54 4.05.05	35.5
4 4 0 4	444	044	9 6 6 9 6	98 98
34 35	36 37 38	39	4 4 4 1 2 8	44 45

### ALIGNMENTS

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Gaps

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Indels

Length 540;

DB 1;

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687D06CB0D70AF91 CRC64;
                                                                                                                           Score 47;
Pred. No.
                            POTENTIAL.
                                                        POTENTIAL.
POTENTIAL.
                 POTENTIAL
                                               POTENTIAL
                                                                           POTENTIAL
                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001940; AAF10437.1; -
                                                                                               59561 MW;
                                                                                                                          42.7%;
                                                                                                                                                                               256 NVPTNIHGLSMDWTGSAL 273
                                                                                                                                                                 1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit
                                                                                              540 AA;
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les 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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2204
2233
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Q9RW10;
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MENG_DEIRA
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(See http://www.lsb-sib.ch/announce/
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). DHAIZ SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hypothetical 59.6 kDa protein in DSR2-CAT8 intergenic region.
                                                                                                                                                                                                                                                     DB 1; Length 1191;
2.2;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                            BA7BB9815431500C CRC64;
                                                                                      EXTRACELLULAR (POTENTIAL).
                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
                                                                   CYTOPLASMIC (POTENTIAL). POTENTIAL.
  CYTOPLASMIC (POTENTIAL).
                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ransport; Transmembrane
                                                                                                                                                                   POLY-PRO.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                    540 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See P
                                                                                                                                                                                                                                                         Score 51; DB 1
Pred. No. 2.2;
2; Mismatches
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                             AA; 129774
                                                                                                                                                                                                                                                                                                             856 TLVFGFKKDWRQALMKD 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRONG, TO YEAST ATRI.
                                                                                                                                                                                                                                                                                                 4 TGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                             MR279C OR YM8021
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                                                                                                                                                                                                                                                                                                                                                                 YM8M_YEAST
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01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Probable S-adenosylmethionine:2-demethylmenaquinone methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiodurans R1.";
Science 286:1571-1577(1999).
-i- FUNCITON: CONVERTS DIMETHYLMENAQUINONE (DMK) TO MENAQUINONE (MK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakacova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                            Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.9%; Score 45; DB 1; Length 160; 50.0%; Pred. No. 2.5; 1.1ve 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 AA; 16860 MW; 54D6F226CA19EC0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).
-!- PATHWAY: LAST STEP IN MENAQUINONE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE MENG FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medigue C., Moszer I., Vlari A., Danchin A.; "Analysis of a Bacilius subtilis genome fragment using a co-operative computer system prototype."; Gene 165:GC37-GC51(1995).
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-168 / JH642;
Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S., Sato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE 12, MEDLINE 12, MEDLINE 1, MEDLINE 12, MEDLINE 13, MEDLINE 13, MEDLINE 14, MEDLINE 14, MEDLINE 15, MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                 Y.;
DNA
                                                                                     Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi "Complete nucleotide sequence of a skin element exclsed by rearrangement during sporulation in Bacillus subtilis."; Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1; Length 284;
Pred, No. 6.7;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; Complete proteome.
32170 MW; F255261D4692ADB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Probable cytochrome C peroxidase (EC 1.11.1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96084975; PubMed-7489895;
              SEQUENCE FROM N.A.
STRAIN-168 / JH642;
MEDLINE-95219086; PubMed-7704261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D32216; BAA06925.1; 1-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D84432; BAA12386.1; -. 299117; CAB14569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.87
Programme 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SubtiList; BG11262; ygaK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 FGWKNDWDAMALK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 protein;
284 AA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 FGLKQDWDGATIK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 299117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHJA OR B3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 28
                                                                                                                                                                                                                                                                                                                          rakeuchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YHJA_ECOLI
P37197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHJA_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + Diffractose 6:phosphate = ADP + D-fructose 1,6-bisphosphate...
-! FATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
-!- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY: TWO DOMAIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update);
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 32:2 kDa protein in SPOIIIC-CWLA intergenic region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propom; PD000707; Phosphofructokinase; 2.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Repeat.
SEQUENCE 756 AA; 83301 MW; 26A89B801D286534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphyldcoccus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.9%; Score 45; DB 1; Best Local Similarity 53.3%; Pred. No. 13;... Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; C50F4.2; CE05467.
INterPro; IPR000023; Phosphofructokinase.
Pfam; PF00365; PFK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z70750; CAA94737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00476; PHFRCTKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 VIGIKHGWDGLKNKD 450
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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GVFGLKQDWDGATI 18
                                         (Phosphohexokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
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P45908;
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SO WERE THE DESCRIPTION OF THE PROPERTY OF THE

YOAK\_BACSU
ID YOAK\_BACSU
AC P45908
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Gaps

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             the European Bioinformatics Institute. There are no restrictions on its use by, non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
    and the EMBL outstation
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1 (COVALENT) (BY SIMILARITY).
1 (HEME PROXIMAL) (BY SIMILARITY).
2 (COVALENT) (BY SIMILARITY).
2 (HEME PROXIMAL) (BY SIMILARITY).
3 (COVALENT) (BY SIMILARITY).
3 (COVALENT) (BY SIMILARITY).
3 (COVALENT) (BY SIMILARITY).
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ON 3 (HEME DISTAL) (BY SIMILARITY).
9F494A698949E6DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 1; Length 465; pred. No. 11; 4; Mismatches 2; Indels
                                                                                                                    Ecodene; EG12244; yhjA.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR00345; CytC_teme_bind.
InterPro; IPR00345; CytCotrome.c: 1.
PROSITE; PS000190; CYTCOTRROME_C; 3.
Hypothetical protein; Oxidoreductase; Peroxidase; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69178 MW; B188DFE02ACC54E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsRNA, viruses; Cystoviridae; Cystovirus
NCBI_TaxID=10879;
between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                   Blectron transport; Complete proteome. --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P11129;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JÄN-1990 (Rel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-13.
                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                              HEME 1
IRON 1
HEME 2
IRON 2
HEME 3
HEME 3
IRON 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                             EMBL;; AE000428; AAC76543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M17462; AAA68485.1; -. PIR; C28648; P3BPF6. Envelope protein SEQUENCE 648 AA; 69178 MW
                                                                                               EMBL; U00039; AAB18494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            40.0%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             VFGLKQDWDG--ATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               || ::| ||| ||::|
243 VFNVEQFWDGRAATLQD 259
                                                                                                                                                                                                                                                                                                                                                      51570
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                          210
210
211
211
354
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterlophage ph1-6.
                                                                                                                                                                                                                                                                                                                                                      465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VР3_ВРРН6
Р11129;
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Best Local C
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SEQUENCE
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BINDING
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                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/potassium-transporting ATPase alpha chain (EC 3.6.3.9) (Sodium pump) (Na+/K+ ATPase)
Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Eukaryota, Metazoa, Arthropoda, Crustacea, Branchiopoda, Anostraca;
                                                                                                                                                                                                                                                                                                                                                          Macias M.T., Martinez J.L., Palmero I., Sastre L.;
"Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES), SUBFAMILY IIC.
                              ..
 Length 648
                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pram; Profession Arpase_C; 1.
Pram; Profession Arpase_C; 1.
Pram; Profession Cation Arpase_N; 1.
Pram; Profession El-E2_Arpase; 1.
Pram; Profession El-E2_Arpase; 1.
Pram; Profession El-E2; 1.
PRINTS; PROfession El-E2; 1.
PROSITE; PSOFOLS; ARPASE_EL-E2; 1.
Hydrolase; Sodium/Poctassium transport; Transmembrane;
DB 1;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                            PRT; 1004 AA
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interpro; IPR004014; Catlon_ATPase.
Interpro; IPR001757; E1-E2_ATPase.
Interpro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-92039032; PubMed-1657719;
Macias M.T., Martinez J.L., Palme
                                                                                                                                                                                        (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X56650; CAA39972.1; -.
    40.0%;
                                                                                       181 IFGWYVKMDWEGSAVAD 197
                                                            6 VFG--LKQDWDGATIKD 20
      Query Match 40.0
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JH0470; JH0470.
HSSP; P04191; 1EUL.
                                                                                                                                                                                                                                                                                             Artemiidae; Artemia
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND GAMMA.
                                                                                                                                                            AT1A_ARTSF
P28774;
                                                                                                                                                                                          01-DEC-1992
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBL\_TaxID=1394;

Bacillus caldolyticus.

MEDLINE-94282293; PubMed-7516791;

SEQUENCE FROM N.A.

STRAIN-DSM 405;

01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CT\_2001 (Rel. 40, Last annotation update)
Dihydroorotase (EC 3.5.2.3) (DHOase).

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STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hisosuchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis ap. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - CATALYTIC ACTIVITY: Shikimate + NADP(+) - 5-dehydroshikimate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%; Score 43.5; DB 1; Length 290; 47.8%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1; Length 1004;
Pred No. 26; 5; Indela
BY SIMILARITY,
BY SIMILARITY,
BY SIMILARITY,
PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                    MW; CE4E6BECE19A78C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002907; Shikimate_DH.
Pfam; PF01488; Shikimate_DH; 1.
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290'AA; 31099'MW; 8A2D38EE5D57B303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 11; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 7290 AA.
                                                                                                                                        ATP (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.(4571)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Shikimate 5-dehydrogenase (EC 1.1.1.25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AROE OR SIR1559.
Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-97061201; Pubmed-8905231;
                                                                                                                                                                1004 AA; 110699
                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AROE SYNY3 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90916; BAA18699.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 LFGLRKHWDSRAVND 878
                                                                                                                                                                                                                                                                                                                                                                                              6 VFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
                                     TRANSMEM
TRANSMEM
MOD_RES
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
   TRANSMEM
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                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AROE_SYNY3
      SEFFF
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                                                                                                                                                                                             1- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P30797/9/
01-0CT-1996 (Rel. 34, Last sequence update),
16-0CT-2001 (Rel. 40, Last annotation update)
Sodium/potassium-transporting Afrase alpha-1 chain precursor
(EC 3.6.3.9) (Sodium pump 1) (Na+/R+ Afrase, 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                      -i- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1; Length 427;
Pred. No. 15;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           759A2AA99F733F4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (POTENTIAL).
ZINC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrimidine biosynthesis; Hydrolase; Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00744; Dihydroorotase; 1:
PROSITE; PS00482; DIHYDROOROTASE_1; 1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002195; Dihydrooratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL 62 62 Z
SEQUENCE 427 AA; 46047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73308; CAA51737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 68.00;
The conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 TGVFTLKQLVDWLTIK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGVFGLKQDWDGATIK 19
                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M38.972
                                                                                                                                                                                                                                                                     aspartate.
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P50997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL .
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105 TNTDVEGFLAPLLELKQDWSGRT 127

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RESULT

2 TTTGVFG-----LKQDWDGAT 17

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715 711
719 71
109 10
185 18
249 24
309 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CJUW OR B4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
YJJW_ECOLI
ID YJJW_ECOLI
AC P39409;
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CONFLICT
CONFLICT
                               MOD_RES
MOD_RES
MOD_RES
FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb'sib.ch/announce/or send an email to license(19b-sib.ch).
                                                                                                                                                                                                                                               -1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME, WHICH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF NA HOLD ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
-1- CATALYTIC ACTIVITY: ATP + H(12)0 + Na(+)(out) - ADP + Phosphate + Na(+)(out) - K(+)(in).
-1- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSITE; PS00154; AFPASE_E1_E2; 1.
ydrolage; Sodium/potassium transport; Transmembrane; Phosphorylation;
agnesium; Metal-binding; ATP-binding; Multigene family.
                                                                                                                                                                            Canessa C.M., Horisberger.J.-D., Louvard D., Rossler B.C.;
"Mutation of a cysteine in the first transmembrane segment of Na.K-
ATPase alpha subunit confers ouabain resistance.";
EMBO J. 11:1681-1687(1992):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
SODIUM/POTASSIUM-TRANSPORTING ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein, SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1.E2 ATPASES). SUBFAMILY IIC.
                                   Xie Z., Li H., Liu G., Wang Y., Askari A., Mercer R.W.;
Cloning of the dog Na/K-Arbase alpha i subunit.",
(In) Bamberg E., Schoner W. (eas..);
The sodium pump, pp.49-52, Springer:Verlag, New York (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUMENAL
                                                                                                                                          TISSUE-Kidney;
MEDLINE-92258376; Pubmed-1316269;
                                                                                                                         SEQUENCE OF 92-307 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               AND GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
Magneslum;
PROPEP
CHAIN
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DOMAIN
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TRANSMEM
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DOMAIN
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PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAPK) (BY
                                                                         SIMILARITY).
BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY BINILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                Length 1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRALT-X12 / MGES5;
MEDLINE-95334362; Dubmed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                              MW; 938A19AA487CBEAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 1;
Pred. No. 39;
2; Mismatches
                                                                                                                                                                                                C -> Y (IN REF. 2
I -> V (IN REF. 2
K -> E (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein 13jW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 AA.
                                                                                                                                                                                                                                                                       (IN REF
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ECOGENE, EG1259; Y19W.
InterPro; IPR001989; Radical_activat.
InterPro; PR001989; Radical_activat.
Pfam; PF00017; fer4; 2;
Pfam; PF02143; Radical_activat; 1.
ProDom; PD004758; Radical_activat; 1.
PROSITE; PS00198; AFEAS.FERREDOXIN; 2.
PROSITE; PS01087; RADICAL_ACTIVATING; 1.
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                                                                                                                                                                                                                                                                                                                                                                        39.18;
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HSSP; P00198; 2FDN:
                                                                                                                                                                                                                                                                                                 112666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TGVFGLKODWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.1
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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143 LCQDWEGATL 152
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
9 LKQDWDGAII 18
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1902;
                                                                                                                                                DNAA_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                        RESULT 14
DNAA_STRCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE—21128732; PubMed-11234002;
Ccle S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor B. Davies R.M., Deviln K., Dutthoy, E., Eiglwell T. Fraeer A., Hensoy T., Jagels K., Lacrolx C., Maclean J., Moule S., Murphy L., Coliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutherford K.M., Rutherford K.M., Rutherford K.M., Rutherford K.M., Rutheres S., Stevens K., Taylor K., Mhitchead S., Woodward J.R., Barrell B.G.;
                                                                                  SIMILARITY)
SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                          (BY SIMILARITY (BY SIMILARITY
                                                                                                                                                SIMILARITY
S; Complete proteome.
(4FE-4S) (BY SIMILARITY)
(4FE-4S) (BY SIMILARITY)
(4FE-4S) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                            Query Match 38.2%; Score 42; DB 1; Length 287; Best Local Similarity 50.0%; Pred. No. 14; Matches 8; Conservative 2; Mismatches 6; Indels
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38.2%; Score 42; DB 1; Length 307;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                  (4FE-4S) (BY (4FE-4S) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. 1 K. 17 . . .
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Bacteria: Firmicutes: Actinobacteria. Actinobacteridae.
                                                                                                                                                                                                                                   RON-SULFUR 2 (4FE-4S) (B. E08BB429519E54B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Complete proteome.
SEQUENCE 307 AA; 32853 MW; EEFE5BA102455DA2 CRC64;
                                                       IRON-SULFUR (4FE-4S) (BY IRON-SULFUR 1 (4FE-4S) (IRON-SULFUR 1 (4FE-4S) (IRON-SULFUR 1 (4FE-4S) (IRON-SULFUR 2 (4FE-4S) (IRON-
                                                                                                                                                                                                               IRON-SULFUR 2 (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1- SIMILARITY: BELONGS TO THE UPPO105 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03.2300.
30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 32.9 kDa protein ML0860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 307 AA.
Iron-sulfur; 4Fe-4S;
                 TRON - SULFUR
                                                                                                                                                                                                                                                       31490 MW;
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                                                                                             3.55
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                                                                                                                                                                                                                                                                                                                                                                                                                              249 GVYGEAQSWASATPED 264
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Hypothetical
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032960;
                                                                                                                                                                                                                                                       SEQUENCE
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YM16_MYCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INTITATION AND REGULATION OF CHROMOSOMAL REPLICATION; PINDS TO THE ORIGIN OF REPLICATION; IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS (DNA BOX) 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO ACIDIC PHOSPHOLIFIDS.

ACIDIC PHOSPHOLIFIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE-92250416; PubMed-1577691;
Calcutt M.J. Schmidt F.J.;
"Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome."
                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
Brown S.P., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL), 6C1D5C0193D3C92B CRC64;
                                                         16-0CT-2001 (Rel. 23, Last sequence update)
Chromosomal replication initiator protein dnaA.
DNAA OR, SCHIB 16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%.. Score 42; DB 1; 36.8%; Pred. No. 35; ative 5; Mismatches
656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1020 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA replication; DNA-binding; ATP-binding NP-BIND 357 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol, 174:3220-3226(1992);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 51-656 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF187159; AAA26734.1; -
                    P27902; Q9KXX4;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequi
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 364 A
656 AA; 73182 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1.
PROSITE; PS01008; DNAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003593; AAA.
Interpro; IPR001957; Bac_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00308; bac_dnaA;
PRINTS; PR00051; DNAA.
STANDARD;
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                                                                                                                                                                                        Streptomyces coelicolor.
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ID Ala2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Featily of human Na+,K+-Arpase genes. Structure of the putative requiratory reglon of the alpha+-gene."; realistory reglon of the alpha+-gene."; 24:481-483(1989).

-!- FEBS.Lett. 244:481-483(1989).

-!- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME, WHICH CATALYZES THE HYDROXYSIS OF ATP COPPLED WITH THE EXCHANGE OF NA AND K 100NS ACRANGE OF NA AND K 100NS ACRADES THE ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.

-!- CATALYTIC ACTIVITY: ATP + K(+)(10) + K(+)(0ut) = ADP + Phosphate + Na(+)(0ut) + K(+)(11).

-:- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hull M.M., Lingrel J.B.;
Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
roc. Natl. Acad. Sci. U.S.A., 84:4039-4043(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The family of human Na+ K+. ATPase genes: No less than five genes and/or pseudogenes related to the alpha-subunit.";
FEBS Lett. 217:275-278(1987).
                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta, and Brain;
MEDLINE-87247232; PubMed-3036582;
Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,
Allikmets R.L., Melkov A.M., Smirov Y.V., Malyshev I.V.,
Dulobova I.E., Petrukhin K.E., Grishin A.V., Kijatkin N.I.,
Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchnikov Y.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-4 FROM N.A.
MEDLINE-89153603; PubMed-2537767;
SYSTGIOV E.D., Bessarab D.A., Malyshev I.V., Petrukhin K.E.,
Smirnov Y.V., Ushkaryov Y.A., Monastyrskaya G.S., Broude N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IIC.
                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last.sequence.update)
16-OCT-2001 (Rel. 40, Last.annotation.update)
Sodium/potassium-transporting Arpsase alpha-2 chain precursor (EC 3.6.3.9) (Sodium pump 2) (Na+/K+ Arpsase 2).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90008924; PubMed-2477373;
Shull M.M., Pugh D.G., Lingrel.J.B.;
"Characterization of the human Na,K-AIPage alpha 2 gene and identification of intragenic restriction fragment length polymorphisms.";
                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 264:17532-17543(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE-87231946; PubMed-3035563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M27571; AAA35575.1; JOINED.
EMBL; M27576; AAA85575.1; JOINED.
EMBL; Y07494; CAA68793.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 211-249 FROM N.A.
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                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                ISSUE-Leukocyte;
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P50993; 007059;
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PRINTS; PRO0119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
PROSITE; PS00154; APPASE_EL_E2; 1.
Hydrolase; Sodium/Potassium transport; Transmembrane; Phosphorylation;
Magnesium; Metal-binding; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
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                                                                                                                                                                                                    SODIUM/POTASSIUM-TRANSPORTING ATPASE
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 1020;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MAGNESIUM (BY SIMILARITY).
W; AFBD8EA94FFB4FC3 CRC64;
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CYTOPLASMIC (POTENTIAL)
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                                                Interpro; IPR001454; Hydrolase.
Interpro; IPR000661; Na_H_K_ATPase.
Pfam; PF00689; Cation_ATPase_C; 1.
Pfam; PF00690; Cation_ATPase_N; 1.
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
                        interPro; IPR004014; Cation_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              718 718
1020 AA; 112265
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Best Local Similarity 40.0%;
Matches 6; Conservative
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HSSP; P04191; 1EUL.
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McBride J.W., Yu, Xj, Walker D.H.; "Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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MEDLINE-98371112; PubMed-9705412;
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-JAKE;
MEDLINE-20432107; PubMed-10974556;
MCBLIde J.W., Yu X.J., Walker D.H.;
A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis.";
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ebrlichieae; Ebrlichia.
NCBL_TaxID=944;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 AA.
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GenCore version 4.5, Copyright (c), 1993 - 2000 Compugen Ltd.
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Match Length
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Result No.

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STRAIN-ARKANSAS;
MEDLINE-98321180; PubMed-9647746;
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SEQUENCE 246 AA; 26884 MW;
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 15; Conserva
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Q9RH35
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                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                               Length 288;
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Rickettsiaceae; chrlichieae; Ehrlichia.
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Rickettslaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID-945;
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280 Aa; 30731 MW; CCAA6C34E2AF393E CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-4.
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Last annotation update)
                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 20; Conservative 0; Mismatches 0;
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MEDLINE-21153566; PubMed-11254561;
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EMBL, U72291; AAC02940.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
                                                                      IPR002566; Surface_Ag_msp4.
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
MAJDR OUTER MEMBRANE PROTEIN OMP-1F.
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                                                                                                  Pfam; PF01617; Surface_Ag_2; 1
SEQUENCE 288 AA; 31590 MW;
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                               EMBL; AF07853; AAC68667.1
EMBL; AF082744; AAG14362.1
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Best Local Similarity 94.49
Matches 17; Conservative
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     Gene 254:245-252(2000)
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052107.
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       5 R R R R R S
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Yu X.J., McBride J.W., Walker D.H.,
"Genetic diversity of the 28-kilodalton outer membrane protein gene in
human isolates of Ehrlichia chaffeensis.";
Clin. Microbiol. 37:1137-1143(1999).
EMBL; AF077735; AAC31548.1;
InterPro; IPR001702; Gram.neg_porin.
InterPro; IPR002566; Surface_Ag_msp4.
                                                        Molecular characterization of a 28 kDa surface antigen gene family of
                                                                                                                                                                                                                                                                                                                                                                              Gaps
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J., Alleman A.R.;
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Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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                                                                                                                                                                                                                                                                                                             Score 90; DB 2; Length 280;
Pred. No. 5e-06;
                                                                                                             Blochem. Blophys. Res. Commun. 247:636-643(1998).
EMBL. AF062761. AAC26720.1;
Interpro. IPRO02566; Surface_Ag_msp4.
Pfam: PF01617; Surface_Ag_2: 1.
SEQUENCE 280 AA; 30743 MW; FBB841DAF08EE4DC CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annot
OUTER MEMBRANE PROTEIN P28 (FRAGMENT)
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MEDLINE-99175287; PubMed-10074538;
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us-10-054-647-2:rspt

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"Molecular characterization of a 28 kDa surface antigen gene family of the tribe Ehrlichiae.";
Biochem. Biophys. Res. Commun. 247:636-643(1998).
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                                                                                                                                                                                                                                   Long S.W., Zhang X.-F., Q1 H., Standaert S., Walker D.H., Yu X.-J. "Allele variation and patterns of transcription of the Ehrlichla Chaffeensis 28 kDs outer membrane protein multigene family."; Submitted (JUN-2001) to the EMBL, Genbank, DDBJ databases. EMBL; AF393393; AAL12923.1; SEQUENCE 276 AA; 30028 MW; 2D7143AFCBFFZEBE CRC64;
                                                                                              Ehrlichia chaffeensis:
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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      093DD1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
001-DEC-REMBRANE PROTEIN P28.
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Best Local Similarity 83.3%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 2;
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70.0%; Pred. No. 8.6e-05;
tive 3; Mismatches 3
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
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MEDLINE-98321180; PubMed-9647746;
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Matches 14; Conservative
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"Genetic diversity of the 28-kilodalton outer membrane protein gene in
human isolates of Bhrlichia chaffeensis.";
J* Clin. Microbiol. 37:1137-1143(1999).
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                                                                                          SIKAIN=V2;
Lindy S.W. Zhang X.-F., Ql. H., Standaert S., Walker D.H., Yu X.-J.;
"Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer.membrane protein multigene family ";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.
"Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 Kob outer membrane protein multigene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF077734; AAC131547.1;
EMBL: AF039395; AAL12025.1;
Interpro: IPR002566; Surface_Ag_msp4.
Pfam: PF01617; Surface_Ag_msp4.
SEQUENCE 276 AA; 30027 MW; 2F03698FCF1F60BE CRC64;
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Pred. No. 2.1e-05;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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Rickettslaceae; Ehrlichleae; Ehrlichia.
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MEDLINE-99175287; PubMed-10074538;
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                    SEQUENCE FROM 'N.A.
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                          NCBI_TaxID=945;
                                                                                  STRAIN-V2;
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Yu X.J., MCBride J.W., Walker D.H.; "Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
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WIX J. W. Melker D.H.;
"Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
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Bacteria; Proteobacteria; alpha subdivision; Rickettslales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Rickettsfaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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Yu X.-J., Walker D.H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF07733; AAC31246.11 -1
Inferpro; IPR0556; Sutface_Ag_msp4.
Pfam; PF0161; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30304 MW; 91C54AC7851B77F2 CRC64;
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00TER MEBBRANE PROTEIN P28.
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Best Local Similarity 77.8%;
Matches 14; Conservative
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                   59 NTTVGVFGLKQNWDGSAISN 78
NTTIGVEGLKQDWDGATIKD 20
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STRAIN-V8, AND V4;
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                                                                                                                                                     STRAIN-ARKANSAS;
MEDLINE-98084465; PubMed-9423849;
Ohashl, N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J., "Allele variation and patterns of transcription of the Ehrlichia chaffeensis 28 kba outer membrane, protein multigene family."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       Ohashi N., Rikihisa Y., Unver A., "Analysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                        Ehrlichia chaffeensis.
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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70.0%; Pred. No. 8.7e-05; Undels
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SEQUENCE 281 AA; 30388 MW; B54DBB55AC839A9A CRC64;
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Interpro; IPRO02566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2: 1. 48995F7C4459AA9A CRC64;
SEQUENCE 281 AA; 30343 MW; A9995F7C4459AA9A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00-DEC-2001 (TrEMBLRel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ARKANSAS;
MEDLINE-21153566; Pubmed-11254561;
       MAJOR OUTER MEMBRANE PROTEIN P28
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Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                               chaffeensis
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MEDLINE-21153566; PubMed-11254561;
Medashi N., Rikhibas Y., Onver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E.
Ehrlichla canis and application of the recombinant protein for serodiagnosis.";
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30803 MW; 27238BE1C7E68A91 CRC64;
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Last annotation update)
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65.0%; Pred. No. 0.00052;
tive 3; Mismatches 4;
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65.0%; Pred. No. 0.00052;
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                                                                                   r. Clin. Microbiol. 36:2671-2680(1998).
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09F473;
01-MAR-2001 (TrEMBLrel. 16, C3
01-MAR-2001 (TrEMBLrel. 16, L6
01-JUN-2001 (TrEMBLrel. 17, L9
P28-6.
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Matches 13; Conservative
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EMSL; AF1933391; AAL12911.1; - TOBDC8710BC167E9 CRC64;
                     Long S.W., Zhang X.-F., Q1 H., Standaert S., Walker D.H., Yu X.-J.; "Allele variation and patterns of transcription of the Ehrlichia deffensis 28 kba outer membrane protein multigene family."; Submitted (JUN-201) to the EMBL/GenBank/DbBJ databases.

EMBL; AF077732; AAC31545.1;
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MEDILINE-89371112; Pubmed-9705412;
MEDILINE-89371112; Pubmed-9705412;
MODASHI N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivísion; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam: PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30277 WW; 91C54AC78507A63F CRC64;
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Last annotation update)
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Pred. No. 0.00012;
2; Mismatches 2;
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Pred. No. 0.00012;
2; Mismatches 2;
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00TER MEMBRANE PROTEIN P28.
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01-UUN-2001 (TIEMBLIEL. 17, LAST Seq
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MAJOR OUTER MEMBRANE PROTEIN P30-2.
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Local Similarity 77.8%;
es 14; Conservative
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Local Similarity 77.8%;
hes 14; Conservative
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MCBride J.W., Yu X.J., Walker D.H.;
McBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis.";
Ehrlichia canis.";
EMBL; AF082744; AAG14361.1; -
InterPro; IPR002566; Surface_Ag_msp4.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=944;
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SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
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